

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

NEB 1233

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-1391      -1381      -1371      -1361      -1351      -1341      -1331      -1321
|          *          *          *          *          *          *          *
AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT CCACTAGTAA
pCR2.1 -BamHI-
Lac promoter
-1311      -1301      -1291      -1281      -1271      -1261      -1251      -1241
*          *          *          *          *          *          *          *
CGGCGGCCAG TGTGCTGGAA TTCGGCTTAC TATAGGCAC GCGTGGTCGA CGGCCGGGC TGGTAACTTT AAGAGAAATT
pCR2.1 -SmaI-
GenomeWalker Adaptor
cmAC01
-1231      -1221      -1211      -1201      -1191      -1181      -1171      -1161
*          *          *          *          *          *          *          *
GGTAAAATTC CTAGAGAGAA TTGTAATTAA TATAGGAGAA TGATTTTAAAT TCTAATGTTG TATCCATTTT CGATAAAGTT
cmAC01 Genomic DNA
-1151      -1141      -1131      -1121      -1111      -1101      -1091      -1081
*          *          *          *          *          *          *          *
AAATAAAGTG TCGTAGACGA CCATCATTCT TAATCCATTT GTACTTATCA AATTGTGATC TGAGATTTAA GTTCAAATTC
cmAC01 Genomic DNA
-1071      -1061      -1051      -1041      -1031      -1021      -1011      -1001
*          *          *          *          *          *          *          *
ACACTAAAAC AATCGAAATG TATGCGACAA TCACAATGGA AAATACGTAT GATGTATTCC ATCACCTTTC AAGTTCTAAC
cmAC01 Genomic DNA
-991      -981      -971      -961      -951      -941      -931      -921
*          *          *          *          *          *          *          *
CTAGGATATG TTTTGAATA TTTGAGATTT ATTAAATTAT TCTTTTATCC GTTGACAGTT TATTTTTTGT TTAACGATGT
cmAC01 Genomic DNA
-911      -901      -891      -881      -871      -861      -851      -841
*          *          *          *          *          *          *          *
ATGTAAGAAA CGACGAAATA TGTGATTAAA CCAAGATCGC ATACAAATAA GAGCTAGATC CTAAAGATAT ATAAAAGTAT
cmAC01 Genomic DNA
-831      -821      -811      -801      -791      -781      -771      -761
*          *          *          *          *          *          *          *
GATCAACAAC GTACAAAACG TTTCTTTTTC ATGATAATTA TCCTAAGAAC TTCAAGGTTA ATTTAGATCT CTTAATTAAA
cmAC01 Genomic DNA
-751      -741      -731      -721      -711      -701      -691      -681
*          *          *          *          *          *          *          *
AAATTCATA GATAATGCAT CCGTGAACAA GAAAAACAT AAAGAACCCA TGGTGTCTCT AATTTTGTGA GTAAATAAGC
cmAC01 Genomic DNA
-671      -661      -651      -641      -631      -621      -611      -601
*          *          *          *          *          *          *          *
GTAGTTC AAG ACACAAGTAA GAATGACGTT ACCACATGTT AATCTAGATT CCAAACTTG AGCTTGAGAG CACGTTACGA
cmAC01 Genomic DNA

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Fig. 1A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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-591      -581      -571      -561      -551      -541      -531      -521
  *        *        *        *        *        *        *        *
AAATAATCTA CGAAAACGAG TAAGTCGTCT AAGTTCGTTT TCGTTTATTT GACACGTAAG ATACTCGTAT TGAAAGAAGA
cmAC01 Genomic DNA>

-511      -501      -491      -481      -471      -461      -451      -441
  *        *        *        *        *        *        *        *
CGAAAAATGG AAAAAAGTAA AGAAGGTAAG GAGGTGGGTG AGTCCAAAGG AAACATACCA AATTCATGCA AGAACTATGA
cmAC01 Genomic DNA>

-431      -421      -411      -401      -391      -381      -371      -361
  *        *        *        *        *        *        *        *
GATTCAGAAA TTAAGAGAAA AGTGTGGAAG TCATGTAAGT AAATTTAAAA TACATATAGG TACTATTTTC TTTCCTTTTC
cmAC01 Genomic DNA>

-351      -341      -331      -321      -311      -301      -291      -281
  *        *        *        *        *        *        *        *
TATTGAAACA AAGAGACCAA GGGGGAATTA GGGTATATGG CATTGGCAGA CATAAAAATA ATAAAGTTAA ATCAAATTGG
cmAC01 Genomic DNA>

-271      -261      -251      -241      -231      -221      -211      -201
  *        *        *        *        *        *        *        *
GTCCCAAAC TACCAAAGAG GAAATTCAGT GTTGAATAAA GCCAATTAGC CAAAGCCAAA GCCAAAGCCA CCTCTCTCT
cmAC01 Genomic DNA>

-191      -181      -171      -161      -151      -141      -131      -121
  *        *        *        *        *        *        *        *
TTCCACATA CATGCATGAA ATTTTCATGG CCCATCTCTT TTATCATCAC ATTTTAAATA ATTTTATCTT CTCTCTCTTC
cmAC01 Genomic DNA>

-111      -101      -91      -81      -71      -61      -51      -41
  *        *        *        *        *        *        *        *
TTCTCTCTCT TCTCTCTCTT CTCTCTCTTC TTCTCTCTCT TTTTAAATC AATTTCTTCC CACTTTCCAA TCCTAAATAA
cmAC01 Genomic DNA>

TATA box
|
-31      -21      -11      -1      10      20      30      40
  *        *        *        *        *        *        *        *
ATTTCACTAT AAATACCCCT TCATTATAAC TTGATCCAAC ACAOCCACCA ACCAAAAACA AAACCTTGAT ACCAAAGAGT
cmAC01 Genomic DNA>

50      60      70      80      90      |
  *        *        *        *        *        |
TCPTTTTCTT TTATTTCAC AAACCAAATC TTGTATCTAC AAAAAGAAAT GGCTGTCTA
TAG AACATAGATG TTTTCTTCC taGcCAGAT
-BamHI-
cmAC01 Genomic DNA

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**Fig. 1B**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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-1289      -1279      -1269      -1259      -1249      -1239      -1229      -1219
  *          *          *          *          *          *          *          *
AGGAAACAGC TATGACCATG ATTACGCCAA GCTTAAGAGA AATTGGTAAA ATTCCTAGAG AGAATTGTAA TTAATATAGG
                                HindIII
_____pUC19_____
                                _____cmAC01 Genomic DNA_____>

-1209      -1199      -1189      -1179      -1169      -1159      -1149      -1139
  *          *          *          *          *          *          *          *
AGAATGATTT TAATTCTAAT GTTGTATCCA TTTTCGATAA AGTTAAATAA AGTGTCTAG ACGACCATCA TTCTTAATCC
                                _____cmAC01 Genomic DNA_____>

-1129      -1119      -1109      -1099      -1089      -1079      -1069      -1059
  *          *          *          *          *          *          *          *
ATTTGTACTT ATCAAATTTG TATCTGAGAT TTAAGTTCAA ATTCACTA AAACAATCGA AATGTATGCG ACAATCACAA
                                _____cmAC01 Genomic DNA_____>

-1049      -1039      -1029      -1019      -1009      -999      -989      -979
  *          *          *          *          *          *          *          *
TGGAAAATAC GTATGATGTA TTCCATCACC TTTCAAGTTC TAACCTAGGA TATGTTTGG AATATTTGAG ATTTATTAAA
                                _____cmAC01 Genomic DNA_____>

-969      -959      -949      -939      -929      -919      -909      -899
  *          *          *          *          *          *          *          *
TTATCTTTT ATCCGTTGAC AGTTTATTTT TTGTTTAACG ATGTATGTAA GAAACGACGA AATATGTGAT TAAACCAAGA
                                _____cmAC01 Genomic DNA_____>

-889      -879      -869      -859      -849      -839      -829      -819
  *          *          *          *          *          *          *          *
TCGCATACAA ATAAGAGCTA GATCCTAAAG ATATATAAAA GTATGATCAA CAACGTACAA AACGTTTCTT TTCGATGATA
                                _____cmAC01 Genomic DNA_____>

-809      -799      -789      -779      -769      -759      -749      -739
  *          *          *          *          *          *          *          *
ATTATCTTAA GAACTTCAAG GTTAATTTAG ATCTCTTAAT TAAAAAATTT CATAGATAAT GCATCCGTGA ACAAGAAAAA
                                _____cmAC01 Genomic DNA_____>

-729      -719      -709      -699      -689      -679      -669      -659
  *          *          *          *          *          *          *          *
ACATAAAGAA CCCATGGTTG TCCTAATTTT TGTAAGTAAAT AAGCGTAGTT CAAGACACAA GTAAGAATGA CGTTACCACA
                                _____cmAC01 Genomic DNA_____>

-649      -639      -629      -619      -609      -599      -589      -579
  *          *          *          *          *          *          *          *
TGTTAATCTA GATTCCAAAA CTTGAGCTTG AGAGCACGTT ACGAAAATAA TCTACGAAAA CGAGTAAGTC GTCTAAGTTC
                                _____cmAC01 Genomic DNA_____>

-569      -559      -549      -539      -529      -519      -509      -499
  *          *          *          *          *          *          *          *
GTTTTCGTTT ATTTGACACG TAAGATACTC GTATTGAAAG AAGACGAAAA ATGGAAAAAA GTAAAGAAGG TAAGGAGGTG
                                _____cmAC01 Genomic DNA_____>

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**Fig. 2A**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

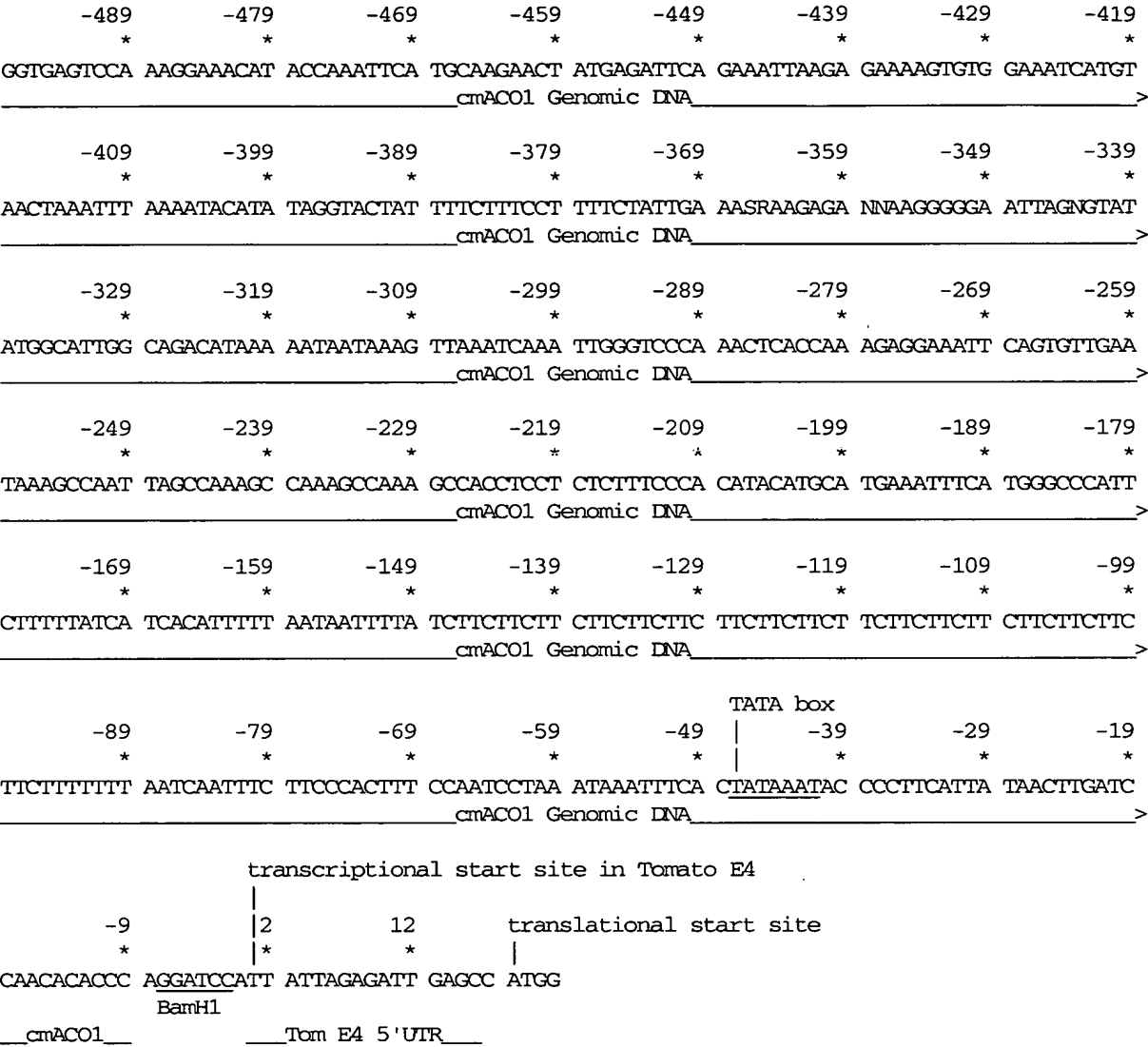


Fig. 2B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

NEB 1233

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-1669      -1659      -1649      -1639      -1629      -1619      -1609      -1599
  *          *          *          *          *          *          *          *
AGGGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT CCACTAGTAA
                                     HindIII          -BamHI-
_____ Lac promoter _____>
_____ pCR2.1 _____>

-1589      -1579      -1569      -1559      -1549      -1539      -1529      -1519
  *          *          *          *          *          *          *          *
CGGCCGCCAG TGTCGTGGAA TTGGGCTTGT AATACGACTC ACTATAGGGC ACGCGTGGTC CACGGCCCGG GCTGGTAACT
_____ pCR2.1 _____>
_____ GenomeWalker Adaptor _____>

-1509      -1499      -1489      -1479      -1469      -1459      -1449      -1439
  *          *          *          *          *          *          *          *
AGAAGCTAAA GGACGACGTC AACATAATTA AAATTACTCC AAGATAAATTA AAATTAAAAA TATCTTATAT TTTATGGCGT
_____ MEL7 promoter _____>

-1429      -1419      -1409      -1399      -1389      -1379      -1369      -1359
  *          *          *          *          *          *          *          *
TACATCTTCC TTCTCTCTTC TTCTTTTTTC TGCTGCGATT TCTTCCCATC TATTCTTCTT TTTACTCTTA TTTTTTTCTT
_____ MEL7 promoter _____>

-1349      -1339      -1329      -1319      -1309      -1299      -1289      -1279
  *          *          *          *          *          *          *          *
TACATIGTTT AGATTTGGGT AACCAAATCT GATTCTTTC TATCGICTTT CTCTCTTTTC TCTTTTTTTT TCGCTGCGA
_____ MEL7 promoter _____>

-1269      -1259      -1249      -1239      -1229      -1219      -1209      -1199
  *          *          *          *          *          *          *          *
TTTCTTCCCA TTGCTATCG TTTTTCCTC TTTTTTTTTT TACATCGTAA CCAAATCTAA AAGATCGTAT ATAAAGAATC
_____ MEL7 promoter _____>

-1189      -1179      -1169      -1159      -1149      -1139      -1129      -1119
  *          *          *          *          *          *          *          *
TTCAAAAAAA AAAATTGTTT AGATTGGAGT AGCCAAATTT AAACAATCGC GTAAAAAATA TAAACGATCG TAGACAAATC
_____ MEL7 promoter _____>

-1109      -1099      -1089      -1079      -1069      -1059      -1049      -1039
  *          *          *          *          *          *          *          *
TAAACGATCG TGCACAAAAA GATTTAATAA AATCGTTTAG TCAAATCTAA ACAATTGTAT AACCAAATTA AACGATAGAA
_____ MEL7 promoter _____>

-1029      -1019      -1009      -999      -989      -979      -969      -959
  *          *          *          *          *          *          *          *
TTGAAATAAT AAATCGGTTA GATTGGCTA TCCAAATTTA AATGACCAA TCTAAACGAT CGTATACCAA ATCTAAACGA
_____ MEL7 promoter _____>

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**Fig. 3A**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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-949      -939      -929      -919      -909      -899      -889      -879
  *        *        *        *        *        *        *        *
TCGKATACCA AATCTAAATG ATCATGTACC AAATATATTA TGCACATTGT TGGCAGGGTG GTTGACGGAA CATTITGTAT
      MEL7 promoter>

-869      -859      -849      -839      -829      -819      -809      -799
  *        *        *        *        *        *        *        *
ATTTTCTATT ATGGGTTTGT AGAATTTTTT CATTITCGAA ATTGTTCTAT ACAATATAAA TATAAATATT TTACCACTTC
      MEL7 promoter>

-789      -779      -769      -759      -749      -739      -729      -719
  *        *        *        *        *        *        *        *
GTTATATTTT CGAAAAGACC CCTTAAATAA ATTGAATTCG CATATAATTA AAATTTTTTC CCAAAAAAAG TAGACTATGT
      MEL7 promoter>

-709      -699      -689      -679      -669      -659      -649      -639
  *        *        *        *        *        *        *        *
CTATCTAAAA ATTTGATTCC CAATATAGAA CAAATTCTCA AAATGAACAA ACATTTGAAA TTCTCGATAT AGAAAACATT
      MEL7 promoter>

-629      -619      -609      -599      -589      -579      -569      -559
  *        *        *        *        *        *        *        *
TACTTATTTT GAATTGGGAC ATATTCCAAA GTTTATTCCA AACGTAACCT TGAAGGAAAA GTTGATTGAG ATTACATCCA
      MEL7 promoter>

-549      -539      -529      -519      -509      -499      -489      -479
  *        *        *        *        *        *        *        *
TATTTTGTIT TTCATATTG AATTCATGG AAAATTAAAA TGCACACAAA ATGATGTATG AGATTAAACC AAAGTTTATC
      MEL7 promoter>

-469      -459      -449      -439      -429      -419      -409      -399
  *        *        *        *        *        *        *        *
GTTATTGAAT TCTTTTATTA AAAAACCAAC AAAATTTTAA AACTTGTTTG CAATAGACCA ATATAGTTAA TCCATCGTGG
      MEL7 promoter>

-389      -379      -369      -359      -349      -339      -329      -319
  *        *        *        *        *        *        *        *
TCTATTGTAG ATAAATTGTA ATATTTTGTT ATATTTAATA AATATTTTGA TTTATTTTGA TATATTTGTA TTTAGATAAC
      MEL7 promoter>

-309      -299      -289      -279      -269      -259      -249      -239
  *        *        *        *        *        *        *        *
AAAATTAAGA TTAAATATT ATTTTATATC TTAATATAAA CATTTGTTAA TTTTCTCTAT TTTAGACCAT TTCTCTTATT
      MEL7 promoter>

-229      -219      -209      -199      -189      -179      -169      -159
  *        *        *        *        *        *        *        *
TTTATATAAC ATTTTAATAA CTAAATGATG TGACACACAC TAATATTATT TTTATCCAAA GAAAATAATG CTATAAAATA
      MEL7 promoter>

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**Fig. 3B**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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      -149      -139      -129      -119      -109      -99      -89      -79
      *         *         *         *         *         *         *         *
TGGGTCCTTCT TTATCAACCTT CATGATAATT ATGAAAAATA AAATAAAATT TAATTATATA ATTCATTTC TCTAATCGTA
_____MEL7 promoter_____>

                        TATA box
      -69      -59      -49      -39      -29      -19      -9      2
      *         *         *         *         *         *         *         *
CAAGCTAGAT ATTACTATAT CAACAACCTTT GTGTATAAAA AGGGCAAGAA ATTAAGCATT ATCGTGTGAG CCACTTTTTC
_____MEL7 promoter_____>

                        Mel7 translational start site
                        |               <cmDruNcoSt
                        |               |
      12      22      32      42      52
      *         *         *         *         *
TATATCTAGA GATAGAAGGT TTAAATCAT GTCTCTAATT GGAAAGCTTG TGAGT
      TTCCA AATTTTgGTA CcGAGAgTAA CCITTCG
                        -NcoI-
_____MEL7 promoter_____>
                        _____MEL7 cds_____>

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**Fig. 3C**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

NEB 1233

-2158 \* -2148 \* -2138 \* -2128 \* -2118 \* -2108 \* -2098 \* -2088 \*

TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTTG GTACCGAGCT

PCR2.1

Lac promoter

-2078 \* -2068 \* -2058 \* -2048 \* -2038 \* -2028 \* -2018 \* -2008 \*

CGGATCCACT AGTAACGGCC GCCAGTGTGC TGGAATTTCG CTTACTATAG GGCACGCGTG GTCGACGGCC CGGGCTGGTC

-SpeI--

PCR2.1

GenomeWalker Adaptor

-1998 \* -1988 \* -1978 \* -1968 \* -1958 \* -1948 \* -1938 \* -1928 \*

CAATCACCGA ACATCATGTT ATGTAGGTGT CGGGAGATGC TACCTATCTG CTGATGTTGG TTCTTTTCTT TGAAAGATAC

MEL2 promoter

-1918 \* -1908 \* -1898 \* -1888 \* -1878 \* -1868 \* -1858 \* -1848 \*

TCTCTGACT TTTTAGTGTG TGCATCTAGA GATGTCCTCT ATTATTTTGA CACCTTTTCT TCTGACGGTG TAGAGCAACA

MEL2 promoter

-1838 \* -1828 \* -1818 \* -1808 \* -1798 \* -1788 \* -1778 \* -1768 \*

CAAAAAATC TTGAATTTCT ATTAAATGGAA TGAGCTATAT CTATACAAAT TGGAACCATA TGACAAATTA AGAAGATTCC

MEL2 promoter

-1758 \* -1748 \* -1738 \* -1728 \* -1718 \* -1708 \* -1698 \* -1688 \*

TTTCTGAATA TTATGCAATA GAAATACTCA CCAGGTGTAA TGATGCACCT TATAGAGAAA ACTTCGACGA ACAAGAGACG

MEL2 promoter

-1678 \* -1668 \* -1658 \* -1648 \* -1638 \* -1628 \* -1618 \* -1608 \*

GCTACTAAGT TTTAGTAGAA TGGGTATTTC TGACCTACTA TGTTTCAGGA TGCGAGGATC TTCATGGTCA ATTGTGACCG

MEL2 promoter

-1598 \* -1588 \* -1578 \* -1568 \* -1558 \* -1548 \* -1538 \* -1528 \*

ATGGTGGAGA ACTGAAAATA TTTOCCATCT CAATGAAATA CTAAACAAC ATATCTTAGA GGTGGAATA TTGATATCT

MEL2 promoter

-1518 \* -1508 \* -1498 \* -1488 \* -1478 \* -1468 \* -1458 \* -1448 \*

AGGGAATACA TTTTATGGGA CCGTTTTCCTA GTTGTTCCGG CAAACACGCA TTCGAGACGG GACGTTTCATG TCGCATACCA

MEL2 promoter

**Fig. 4A**



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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-1438      -1428      -1418      -1408      -1398      -1388      -1378      -1368
  *          *          *          *          *          *          *          *
CGGAGGATCC GCATGTAAGC TATCCAAGCA ATACTTCTAC CCTTTTGTG TTCTTTAATA ATATATTTT TACTTACTAA
MEL2 promoter>

-1358      -1348      -1338      -1328      -1318      -1308      -1298      -1288
  *          *          *          *          *          *          *          *
GATAGTTTCT AAATTTGTG TAGAATCGAA TGCTGGAAGT TCAGTCTAG CTTACCTCAG TGGGTACTTA GCCACTCTCT
MEL2 promoter>

-1278      -1268      -1258      -1248      -1238      -1228      -1218      -1208
  *          *          *          *          *          *          *          *
GGGACAAGA TATGCGAGAT GCGTTGGAT AGACGATTGG ACTACTCAA AGGCCTTGGT TGGGGACCTA AGTCTAGGGC
MEL2 promoter>

-1198      -1188      -1178      -1168      -1158      -1148      -1138      -1128
  *          *          *          *          *          *          *          *
CCACAAGACG GCCAGTGTGA GTAGTTCCAC GACCTCATGT TTGTAGTCCA CGGTAGAGCT CCAATTATGG ACTAAGCTTG
MEL2 promoter>

-1118      -1108      -1098      -1088      -1078      -1068      -1058      -1048
  *          *          *          *          *          *          *          *
ATCAAGCTGT GCAACGGATT GAAGAACAAA CAAGAAATCA CGATGCGTTA GCTTCAAAAG TGAATGAAT GTGAAAGTTC
MEL2 promoter>

-1038      -1028      -1018      -1008      -998      -988      -978      -968
  *          *          *          *          *          *          *          *
ATAGAAGACA TGAGTCGGGC ACAGTAAGGA CCACAACATT ATCTTTAGCT TTGCGATACG TATANNATTT TCCATTATTC
MEL2 promoter>

-958      -948      -938      -928      -918      -908      -898      -888
  *          *          *          *          *          *          *          *
TTAAGTTTTT GAATTACAGT ATTCAGTGAT GATATGCATA TATATGTACC AAACGTAGCC ACTTTTGTAT AATTGTAGGA
MEL2 promoter>

-878      -868      -858      -848      -838      -828      -818      -808
  *          *          *          *          *          *          *          *
CCTGTGGTGT AGAATGGCAT ATGAGGCTCG TTTAAAGACA TACGATTTTC TTTTGCTTTT TTTTAACGAG GAATATTTTT
MEL2 promoter>

-798      -788      -778      -768      -758      -748      -738      -728
  *          *          *          *          *          *          *          *
TATTTGTATT ATGAACTTTA TTACATTCTT TGAATTTCTT TGTATTATGA AGATTTAATT TTTTGTGAA TTTTGTTTG
MEL2 promoter>

-718      -708      -698      -688      -678      -668      -658      -648
  *          *          *          *          *          *          *          *
TATTTTGTA TTTACTAATT TATTTTAAAT TTTCTTTAAT TGAATCGATA ACGAATGCAA ATATTTTACG AAAAAAAGTT
MEL2 promoter>

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**Fig. 4B**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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-638      -628      -618      -608      -598      -588      -578      -568
  *          *          *          *          *          *          *
ATAGGAAAAT ATTTCAAAAA AATAAAAAAT TACATATTTA AAATATTTTT CGACGCATTA CATATGTGGA AAATATGGTG
      MEL2 promoter_____>

-558      -548      -538      -528      -518      -508      -498      -488
  *          *          *          *          *          *          *
CAAACATCAC ATCGGGGATG GTTATTACCG ACGCATGAAT GACACCGAAT ATATAAACGT AAGGAATAGT TATTCCTGAC
      MEL2 promoter_____>

-478      -468      -458      -448      -438      -428      -418      -408
  *          *          *          *          *          *          *
GCATAACTGC TGTCCGAACT GTGGAAGTTA GTTCTCGACA TTATTAACAC TTACGTGAC GTTTTTATGC ATCGGGAGTC
      MEL2 promoter_____>

-398      -388      -378      -368      -358      -348      -338      -328
  *          *          *          *          *          *          *
GCTCCACTTC TTGTAGTGAA GAAATTTTGC CTATAATGTC GGTTTAAAC CGACATTAAA GGCCAAATTT CTTCCTAGTC
      MEL2 promoter_____>
      _____Imperfect inverted repeat_____

-318      -308      -298      -288      -278      -268      -258      -248
  *          *          *          *          *          *          *
ATAATCAATA TMCAAAAGTT CAATTCCAAA AATTACATTT CTCTAGAAAT TCCGTGTGAA CAATTGTCAT AAAGGTTTTA
      MEL2 promoter_____>

-238      -228      -218      -208      -198      -188      -178      -168
  *          *          *          *          *          *          *
AGTGAATTGA AAATTTCAAA ACGTAATTGG ATTAAGCGAG AAAATTATTT TAATCACCAT TCAAAAGTTA TTAACAATGA
      MEL2 promoter_____>

-158      -148      -138      -128      -118      -108      -98      -88
  *          *          *          *          *          *          *
AAAATATGGA AGATAAGATT TCAAAATTAC GTAATTTACT TCTACGTTTC TTTCTTTCCC CTTTAGTAAC TTCACTCATA
      MEL2 promoter_____>

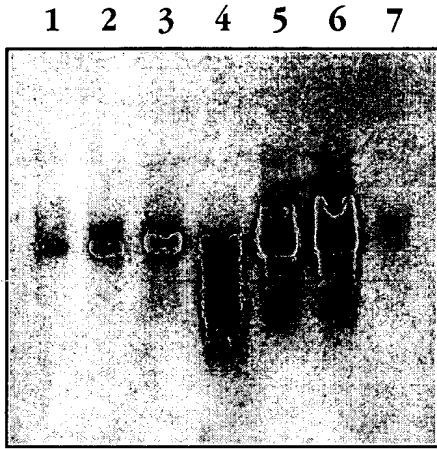
TATA box
| -78      -68      -58      -48      -38      -28      -18      -8
|  *          *          *          *          *          *          *
TCTTTATATA CGTTCCATCC CTTACATTTC TCATACAAAA TTCTCTTTCA ATATCAACTC TCCTCTCTTA ACTCACCCCT
      MEL2 promoter_____>

MEL2 translational start site
|          <MEL2_Nco_R
1 3          13 |
* *          * |
TTTTCAAATG GAAACAATGC AAAC
AAAGggTAC CTTTGTTACG TTIG
-NcoI--
__pro__
      MEL2 cds_____

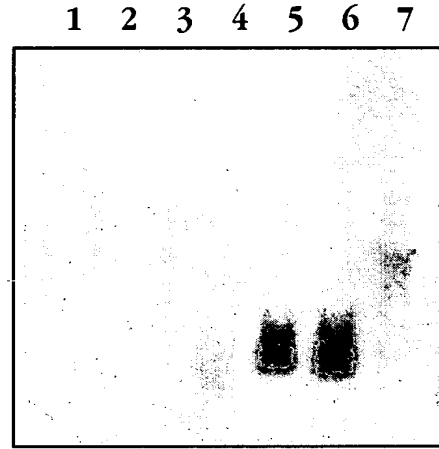
```

**Fig. 4C**

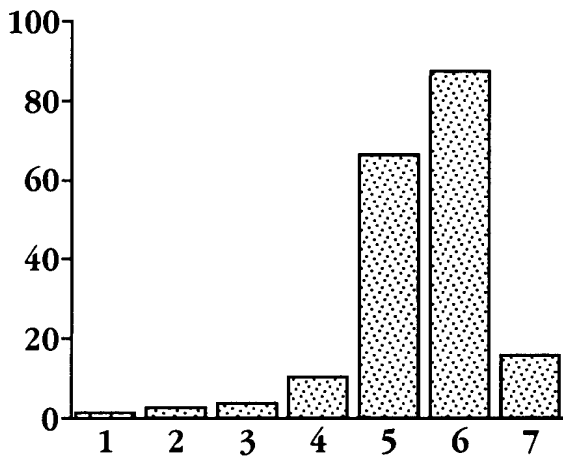
APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		



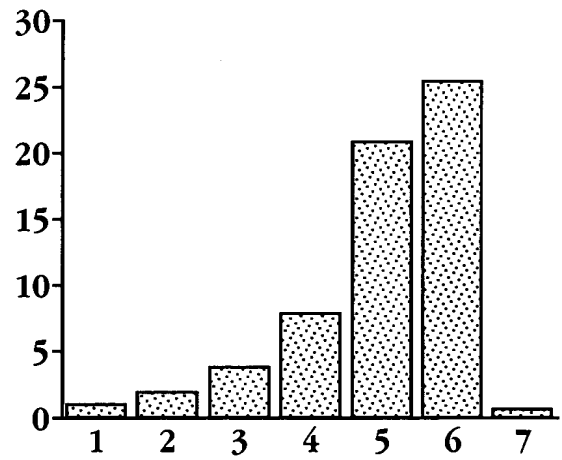
**Fig. 5A**



**Fig. 5C**



**Fig. 5B**



**Fig. 5D**

APPROVED BY	O.G. FIG.
DRAFTSMAN	CLASS SUBCLASS

```

-968      -958      -948      -938      -928      -918      -908      -898
  *         *         *         *         *         *         *         *
TGGAATTGTG AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT
                                                    BamHI>
_____pCR2.1_____>
_____Lac promoter_____>

-888      -878      -868      -858      -848      -838      -828      -818
  *         *         *         *         *         *         *         *
CCACTAGTAA CGGCCGCCAG TGTGCTGGAA TTCGGCTTAC TATAGGGCAC GCGTGGTCGA CGGCCCGGGC TGGTAAATTT
_____pCR2.1_____
_____GenomeWalker Adaptor_____>
_____6E_____>

-808      -798      -788      -778      -768      -758      -748      -738
  *         *         *         *         *         *         *         *
TGAAAAGTTA GGAGATATTT TTTACATATA AGAGATATTT TTTATAATGT AACATTTTTT TTAAGTAGAC GTTGAGTCTGA
_____6E melon genomic DNA_____>

-728      -718      -708      -698      -688      -678      -668      -658
  *         *         *         *         *         *         *         *
GTTAGGTTAA AGAAAGGAAA ACTATAAAAT AATTTTAAAT TATTAAATAC ATAAACAATA CTTTGTATTC TATATTAATT
_____6E melon genomic DNA_____>

-648      -638      -628      -618      -608      -598      -588      -578
  *         *         *         *         *         *         *         *
AAAATGACTA TTGAATTGTT AAGATGTAGG TATCTAAGGA CAAGAAGTCT CGAGTTCAAA TCTTCAACCT CAAAATATAC
_____6E melon genomic DNA_____>

-568      -558      -548      -538      -528      -518      -508      -498
  *         *         *         *         *         *         *         *
TGCAAGATAG TAACTAATGA ATTATATTTG ACTAAATCAT GTAGCAAAAG AAAATCAAAT TTATCATGTT AAATATGGTC
_____6E melon genomic DNA_____>

-488      -478      -468      -458      -448      -438      -428      -418
  *         *         *         *         *         *         *         *
AAGCCGGAGC ATTAACAACA ACAATTCATA TTTGTGGTTG ATAGTACTTG ACTAGAATTT AGAGAGTACT TGACTAGAAT
_____6E melon genomic DNA_____>

-408      -398      -388      -378      -368      -358      -348      -338
  *         *         *         *         *         *         *         *
AAAAATTGGG GGACCCACTA CGACGTCAGC TTGCCTTGCT TAGCAATTAA GCTATCACCT CTTAGTCTAT AGCTTCGTGC
_____6E melon genomic DNA_____>

```

**Fig. 6A**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

```

-328      -318      -308      -298      -288      -278      -268      -258
  *        *        *        *        *        *        *        *
GCTGCATTAA ACGGTATTCT CACACTTTTC TTTTCTTTTT ACOGCACCCG TCCGGTTAAT GGCTCCCCCA CTTTITACCT
_____6E melon genomic DNA_____>

```

```

-248      -238      -228      -218      -208      -198      -188      -178
  *        *        *        *        *        *        *        *
TCCCCGAATC CACGCCAGTT GCCAACATGC GAAGCAGCAA GTACAATATT GTCATTTTGC ATTAACCAAA ATGACACGTC
_____6E melon genomic DNA_____>

```

TATA

box>

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-168      -158      -148      -138      -128      -118      -108      -98
  *        *        *        *        *        *        *        *
GGATGTCATT TATGTAATT AGCTACAAAG CCACGGTTAG TTTCGGAACC CCCACGATCC AGTACTTACG TGCTCTCTAT
_____6E melon genomic DNA_____>

```

```

-88      -78      -68      -58      -48      -38      -28      -18
  *        *        *        *        *        *        *        *
AAATCTTAGA AGCAACGCTT TTACCGGAAT CAACTCATTG GGTATCCCAT TTTCATCTAT CAATTCACCC TTGAAACTGC
_____6E melon genomic DNA_____>

```

6E translational start site

|  
<6EMelNcoP

```

-8      1 3      |
  *      * *      |
TTTTCCCGGC ACOGACT ATG GCC TC
AAAAGGGCCG aGGCTGg TAC CGG A
      --NcoI--
_____6E melon genomic DNA_____

```

**Fig. 6B**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

```

-2442      -2432      -2422      -2412      -2402      -2392      -2382      -2372
  *          *          *          *          *          *          *          *
AAGCTTGCAT GCCTGCAGGT CGACTCTAGA TCAATCAAAC ATTTATTTAA ATAGAACGTT TTAGTGGTTT TTGGATTTTA
-Hind3

pUC-19      >
                2F melon genomic DNA      >

-2362      -2352      -2342      -2332      -2322      -2312      -2302      -2292
  *          *          *          *          *          *          *          *
TTTATCTTTT TTATTATTAA CATTC AATTT AGATTAACT CTTCGAGAAG ATGGAGGAAG AGAATTTTAA GAAATTGAAC
                2F melon genomic DNA      >

-2282      -2272      -2262      -2252      -2242      -2232      -2222      -2212
  *          *          *          *          *          *          *          *
TGAAATAGAC TTAATTATTA AAAATCAAAA GAAAAATGGT GCCAACAAAAG GTGACTAAGA GIGTAATGAA TTGGAATTAG
                2F melon genomic DNA      >

-2202      -2192      -2182      -2172      -2162      -2152      -2142      -2132
  *          *          *          *          *          *          *          *
AACTTTCCCTT CTGTATAGAT ATAATTGATG TTTTCCTTAA CTTTATTTT ATGGTGGTTA TTTATTAAATA ACTGAATTTT
                2F melon genomic DNA      >

-2122      -2112      -2102      -2092      -2082      -2072      -2062      -2052
  *          *          *          *          *          *          *          *
TAAGAGTTCT TTTAATAAACC AAATGTTATA GGATTCAATT GATTGTTTAA TGAGATTAGG CAAACACTTT ATATTGGAGA
                2F melon genomic DNA      >

-2042      -2032      -2022      -2012      -2002      -1992      -1982      -1972
  *          *          *          *          *          *          *          *
AATAATTTAG TGTAGAAAGT AATTTTCATT TTGGATTGTT TAGATGAACA TCAAATCTTG CAACAACATT CAGTTAAGTA
                2F melon genomic DNA      >

-1962      -1952      -1942      -1932      -1922      -1912      -1902      -1892
  *          *          *          *          *          *          *          *
TATATAAATA TATAGAGCCA CCAACCTCAA ATACAATATC TTCGGAAGCA AAATATTATA CATAATATGG AAAGAAGAGT
                2F melon genomic DNA      >

-1882      -1872      -1862      -1852      -1842      -1832      -1822      -1812
  *          *          *          *          *          *          *          *
AGTACTGGTA CATGAATCTT ACGAAGAATT TAAGTATTAT TGGCTTTTCC AATGCAGAAG TCTCAACAAA TCACATTTTA
                2F melon genomic DNA      >

-1802      -1792      -1782      -1772      -1762      -1752      -1742      -1732
  *          *          *          *          *          *          *          *
AAAACCGATT GAATAAACAT GCAAGTAAGA CTTTGTAAAA AACAGCATT CAAACCTCAT ATCAATTATC TCTATATGCA
                2F melon genomic DNA      >

-1722      -1712      -1702      -1692      -1682      -1672      -1662      -1652
  *          *          *          *          *          *          *          *
AAATGTTAGG TCAAATGAGT AATGAAATTA AGGACAAATC AACTAAAAAG AATCAATAAA GTGAATCGAA AAGAAACAAA
                2F melon genomic DNA      >

```

**Fig. 7A**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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-1642      -1632      -1622      -1612      -1602      -1592      -1582      -1572
  *          *          *          *          *          *          *          *
TATCAATCAA ACCTAATGTA TACGTGATTG ATGATGCAGT GTGTTTTGAG ATATGGACAT TTTGATAAAC AACAAACCTC
2F melon genomic DNA>

-1562      -1552      -1542      -1532      -1522      -1512      -1502      -1492
  *          *          *          *          *          *          *          *
CACTCCAATA CGAGAAGAGA GGCATTGAGT GACAGATTAG TGCCCTATTG AAGAGGGTAA GTCCAAAACA AAACAAACAC
2F melon genomic DNA>

-1482      -1472      -1462      -1452      -1442      -1432      -1422      -1412
  *          *          *          *          *          *          *          *
AAAACATGGT GAAGAAATGT TATGAATAAA TGGCAGGGAA AGACATGGTT GTACATGTGG TGTGAGTTTT CTCTTTTCAA
2F melon genomic DNA>

-1402      -1392      -1382      -1372      -1362      -1352      -1342      -1332
  *          *          *          *          *          *          *          *
ATCTGTGAAT AAATTGGATT ACGACCCAAC AAGAGAAACA CTGTTTGGA ACCATGACAG GGCTACCCCA TGGCGTGAAT
-NcoI-
2F melon genomic DNA>

-1322      -1312      -1302      -1292      -1282      -1272      -1262      -1252
  *          *          *          *          *          *          *          *
ATCAAGTATT TAATTAATTA AGCTCTCATC CCCGCCATTC GTTTTTTTAT TCGATTGATA TCTTATATTT TATATACGAA
2F melon genomic DNA>

-1242      -1232      -1222      -1212      -1202      -1192      -1182      -1172
  *          *          *          *          *          *          *          *
TAATCTTGA GTTTGATTTC AATTTAGTTC GTCAATAGTA ATATTTTAAA CTATGTTAAT ATATAAAAAG TAAATGCGAA
2F melon genomic DNA>

-1162      -1152      -1142      -1132      -1122      -1112      -1102      -1092
  *          *          *          *          *          *          *          *
TGATTCTATT AGTATTCACT TTATATCACT CCTTCTTAGA GTAAAGTTTT TAAAGTGGGA AGGGAAATGG AATACGACGT
2F melon genomic DNA>

-1082      -1072      -1062      -1052      -1042      -1032      -1022      -1012
  *          *          *          *          *          *          *          *
GTGATTGGTA GTTAAATTTC CTTATCGACG AGGTTACTGT TTCCTTACTT ATATATATGG AGTCATCCTC AATTTTTCAA
2F melon genomic DNA>

-1002      -992      -982      -972      -962      -952      -942      -932
  *          *          *          *          *          *          *          *
CTCTCAACTT CCAATTATAC AAGCAAAACA TTCAATACCA TACATGCATC TTTTGTAGAA GAAAAGAAGT TCTCTCTTGG
2F melon genomic DNA>

-922      -912      -902      -892      -882      -872      -862      -852
  *          *          *          *          *          *          *          *
ACTTTTTTTT TCAATTCAAC TATGCACCTT TGTTATTTTA GTTTTATAAT TTTTGTGTGT TCTTCCGTTT AATCAAGTTG
2F melon genomic DNA>

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**Fig. 7B**

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

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-842      -832      -822      -812      -802      -792      -782      -772
  *        *        *        *        *        *        *        *
TTGTAATCAA CTTTATGTAT TCAAACACAT AGATAATTTTG TTTAATAGTA TCAGTATATA ATAGGGTTAG AATAACCTTT
-----
                                2F melon genomic DNA>

-762      -752      -742      -732      -722      -712      -702      -692
  *        *        *        *        *        *        *        *
CAAATATGTG TTTTAAAAA ATCAAATCAC TTTAAAAATT AAAATATGTT TAATTAGTGT ATGTTTTTCT TTTTAAGTAT
-----
                                2F melon genomic DNA>

-682      -672      -662      -652      -642      -632      -622      -612
  *        *        *        *        *        *        *        *
TAAACCACGA TAAAAAGTGC TTTAACACTT ATAAAAAATT AGATTAATTT AAAGGAAGTT GTCTGAACGG CAAAATTGAC
-----
                                2F melon genomic DNA>

-602      -592      -582      -572      -562      -552      -542      -532
  *        *        *        *        *        *        *        *
AAAATATAAC AAAGTTTAAT GAACATTGTT CGAAATGTTT CGAAGAGGAA AGAAAAACATT AAGTTTGAAA TATCTCGAGT
-----
                                2F melon genomic DNA>

-522      -512      -502      -492      -482      -472      -462      -452
  *        *        *        *        *        *        *        *
TAAATACATA TCATCCCATG GTAATATATA ACAAACAAA CTTAATCTG AAAAAAAAT TGATGTTAAT AAGAAAAAGA
-----
                                2F melon genomic DNA>

-442      -432      -422      -412      -402      -392      -382      -372
  *        *        *        *        *        *        *        *
GATCAAATC TTAATTTTTT AAAAAAATAA TGGTGAAAAA AACTGAAAAT TTTCCAATAT TGTTTAATTT CAAATTGATC
-----
                                2F melon genomic DNA>

-362      -352      -342      -332      -322      -312      -302      -292
  *        *        *        *        *        *        *        *
CAAAAATTAA AGTTAAAAA GCATTAAACA AAACAATTCA AAACCTAGCT ACTACACATT TACGAAAAATA TATGATACAC
-----
                                2F melon genomic DNA>

-282      -272      -262      -252      -242      -232      -222      -212
  *        *        *        *        *        *        *        *
AAAGGATTTT TGGGTGTAAA CATCTTTTTT ATTTTATATA CACCAAACCT CGTATATATT CACACATAAA GAAGGAAAAA
-----
                                2F melon genomic DNA>

-202      -192      -182      -172      -162      -152      -142      -132
  *        *        *        *        *        *        *        *
GAATTAATGC AAGGGTGTGG CCAATTACGT ACCGTCGTCA TATCTACTC ATCCGTTACG TTCTCAAATC TCTCTCTCTC
-----
                                2F melon genomic DNA>

-122      -112      -102      -92      -82      -72      -62      -52
  *        *        *        *        *        *        *        *
CCTGCTCTCC TAATTATTTC TGCCAGCGAC CATATTTTCAT TTTCAAATTG GTGTTTAAAA AGCCGAGAAT CGCAATCCTT
-----
                                2F melon genomic DNA>

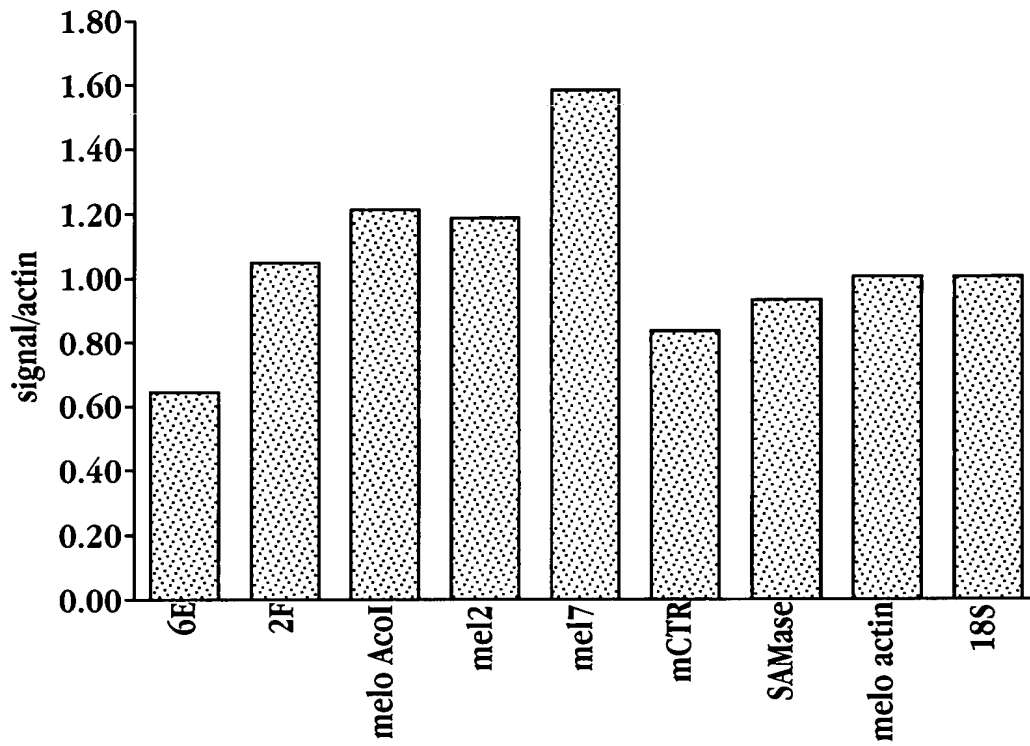
                                Translational start site
-42      -32      -22      -12      -2
  *        *        *        *        *
TTTCTCCAC TCTTAATCA TTCCAATTC AAAAAAT A G GATCGCCAC CATGG
                                |
                                -BamHI- -NcoI-
-----
                                2F melon genomic DNA>

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**Fig. 7C**



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		



**Fig. 8**